

**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 10/539,396

CRF Edit Date: 6/29/05
Edited by: sz

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: invalid beginning/end-of-file text ; page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



PCT

RAW SEQUENCE LISTING

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,396

TIME: 16:08:31

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06292005\J539396.raw

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3 <110> APPLICANT: Tang, Lan
4      Wu, Wenping
5      Duan, Junxin
6      Johannesen, Pia Francke
8 <120> TITLE OF INVENTION: Thermostable alpha-amylases
10 <130> FILE REFERENCE: 10348.204-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/539,396
C--> 12 <141> CURRENT FILING DATE: 2005-06-16
12 <160> NUMBER OF SEQ ID NOS: 6
14 <170> SOFTWARE: PatentIn version 3.3
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 18
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Primer AM298-CDSF
24 <400> SEQUENCE: 1
25 tatcatgaaa ttcagcat                                     18
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 19
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Primer AM298-CDSR
36 <400> SEQUENCE: 2
37 agttcaaaat ggacaaagt                                     19
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 1438
42 <212> TYPE: DNA
43 <213> ORGANISM: Rhizomucor pusillus
46 <220> FEATURE:
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (5)..(1417)
50 <220> FEATURE:
51 <221> NAME/KEY: sig_peptide
52 <222> LOCATION: (5)..(68)
54 <220> FEATURE:
55 <221> NAME/KEY: mat_peptide
56 <222> LOCATION: (68)..()
58 <400> SEQUENCE: 3
59 tatc atg aaa ttc agc atc tct ctc tcg gca gca att gta ctc ttc gcg   49
60      Met Lys Phe Ser Ile Ser Leu Ser Ala Ala Ile Val Leu Phe Ala
61      -20                -15                -10

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63	gcc	gca	aca	agc	ctt	gca	agc	cct	ttg	ccc	caa	cag	cag	cga	tat	ggc	97
64	Ala	Ala	Thr	Ser	Leu	Ala	Ser	Pro	Leu	Pro	Gln	Gln	Gln	Arg	Tyr	Gly	
65	-5				-1	1				5						10	
67	aaa	aga	gca	act	tcg	gat	gac	tgg	aaa	agc	aag	gcc	att	tat	cag	ctg	145
68	Lys	Arg	Ala	Thr	Ser	Asp	Asp	Trp	Lys	Ser	Lys	Ala	Ile	Tyr	Gln	Leu	
69					15				20					25			
71	ctt	aca	gat	cga	ttt	ggc	cgc	gcc	gat	gac	tca	aca	agc	aac	tgc	tct	193
72	Leu	Thr	Asp	Arg	Phe	Gly	Arg	Ala	Asp	Asp	Ser	Thr	Ser	Asn	Cys	Ser	
73				30				35					40				
75	aat	tta	tcc	aac	tac	tgt	ggg	ggg	acc	tac	gaa	ggc	att	acg	aag	cat	241
76	Asn	Leu	Ser	Asn	Tyr	Cys	Gly	Gly	Thr	Tyr	Glu	Gly	Ile	Thr	Lys	His	
77		45					50					55					
79	ctt	gac	tac	att	tcc	ggg	atg	ggc	ttt	gat	gct	atc	tgg	ata	tcg	cca	289
80	Leu	Asp	Tyr	Ile	Ser	Gly	Met	Gly	Phe	Asp	Ala	Ile	Trp	Ile	Ser	Pro	
81		60				65					70						
83	att	ccc	aag	aac	tcg	gat	gga	ggc	tac	cac	ggc	tac	tgg	gct	aca	gat	337
84	Ile	Pro	Lys	Asn	Ser	Asp	Gly	Gly	Tyr	His	Gly	Tyr	Trp	Ala	Thr	Asp	
85	75				80				85			90					
87	ttc	tac	caa	cta	aac	agc	aac	ttt	ggg	gat	gaa	tcc	cag	ctc	aaa	gcg	385
88	Phe	Tyr	Gln	Leu	Asn	Ser	Asn	Phe	Gly	Asp	Glu	Ser	Gln	Leu	Lys	Ala	
89				95				100					105				
91	ctc	atc	cag	gct	gcc	cat	gaa	cgt	gac	atg	tat	gtt	atg	ctt	gat	gtc	433
92	Leu	Ile	Gln	Ala	Ala	His	Glu	Arg	Asp	Met	Tyr	Val	Met	Leu	Asp	Val	
93			110				115					120					
95	gta	gcc	aat	cat	gca	ggg	ccc	acc	agc	aat	ggc	tac	tcg	ggg	tac	aca	481
96	Val	Ala	Asn	His	Ala	Gly	Pro	Thr	Ser	Asn	Gly	Tyr	Ser	Gly	Tyr	Thr	
97		125				130					135						
99	ttc	ggc	gat	gca	agt	tta	tat	cat	cct	aaa	tgc	acc	ata	gat	tac	aat	529
100	Phe	Gly	Asp	Ala	Ser	Leu	Tyr	His	Pro	Lys	Cys	Thr	Ile	Asp	Tyr	Asn	
101		140				145					150						
103	gat	cag	acg	tct	att	gag	caa	tgc	tgg	gtt	gct	gac	gag	ttg	cct	gat	577
104	Asp	Gln	Thr	Ser	Ile	Glu	Gln	Cys	Trp	Val	Ala	Asp	Glu	Leu	Pro	Asp	
105	155				160				165			170					
107	att	gac	act	gaa	aat	tct	gac	aac	gtg	ggc	att	ctc	aac	gac	atc	gtc	625
108	Ile	Asp	Thr	Glu	Asn	Ser	Asp	Asn	Val	Ala	Ile	Leu	Asn	Asp	Ile	Val	
109				175				180				185					
111	tcc	ggc	tgg	gtg	ggg	aac	tat	agc	ttt	gac	ggc	atc	cgc	att	gat	act	673
112	Ser	Gly	Trp	Val	Gly	Asn	Tyr	Ser	Phe	Asp	Gly	Ile	Arg	Ile	Asp	Thr	
113			190					195				200					
115	gtc	aag	cat	att	cgc	aag	gac	ttt	tgg	aca	ggc	tac	gca	gaa	gct	gcc	721
116	Val	Lys	His	Ile	Arg	Lys	Asp	Phe	Trp	Thr	Gly	Tyr	Ala	Glu	Ala	Ala	
117		205				210					215						
119	ggc	gta	ttc	gca	act	gga	gag	gtc	ttc	aat	ggg	gat	ccg	ggc	tac	gtt	769
120	Gly	Val	Phe	Ala	Thr	Gly	Glu	Val	Phe	Asn	Gly	Asp	Pro	Ala	Tyr	Val	
121		220				225					230						
123	gga	cct	tat	caa	aag	tac	ctg	cca	tct	ctc	atc	aat	tac	cca	atg	tat	817
124	Gly	Pro	Tyr	Gln	Lys	Tyr	Leu	Pro	Ser	Leu	Ile	Asn	Tyr	Pro	Met	Tyr	
125	235				240					245			250				
127	tac	gct	ttg	aac	gac	gtc	ttt	gta	tcc	aaa	agc	aaa	gga	ttc	agc	cgc	865

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128 Tyr Ala Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg
129                255                260                265
131 atc agc gaa atg cta gga tca aat cgc aat gcg ttt gag gat acc agc      913
132 Ile Ser Glu Met Leu Gly Ser Asn Arg Asn Ala Phe Glu Asp Thr Ser
133                270                275                280
135 gta ctt aca acg ttt gta gac aac cat gac aat ccg cgc ttc ttg aac      961
136 Val Leu Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn
137                285                290                295
139 agt caa agc gac aag gct ctc ttc aag aac gct ctc aca tac gta ctg      1009
140 Ser Gln Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu
141                300                305                310
143 cta ggt gaa ggc atc cca att gtg tat tat ggt tct gag caa ggt ttc      1057
144 Leu Gly Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe
145 315                320                325                330
147 agc gga gga gcg gat cct gct aac cgt gaa gtg ctg tgg acc acc aat      1105
148 Ser Gly Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn
149                335                340                345
151 tat gat aca tcc agc gat ctc tac caa ttt atc aag aca gtc aac agt      1153
152 Tyr Asp Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser
153                350                355                360
155 gtc cgc atg aaa agc aac aag gcc gtc tac atg gat att tat gtt ggc      1201
156 Val Arg Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly
157                365                370                375
159 gac aat gct tac gcc ttc aag cac gcc gat gct ttg gtt gtt ctc aat      1249
160 Asp Asn Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn
161                380                385                390
163 aac tat gga tca ggt tcc aca aac caa gtc agc ttc agc gtt agt ggc      1297
164 Asn Tyr Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly
165 395                400                405                410
167 aag ttc gat agc ggc gca agc ctc atg gat att gtc agt aac att acc      1345
168 Lys Phe Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr
169                415                420                425
171 acc acg gtg tcc tcg gat gga aca gtc act ttc aac ctt aaa gat gga      1393
172 Thr Thr Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly
173                430                435                440
175 ctt ccg gct atc ttc acc tct gct taactttgtc cattttgaac t      1438
176 Leu Pro Ala Ile Phe Thr Ser Ala
177                445                450
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 471
182 <212> TYPE: PRT
183 <213> ORGANISM: Rhizomucor pusillus
185 <400> SEQUENCE: 4
187 Met Lys Phe Ser Ile Ser Leu Ser Ala Ala Ile Val Leu Phe Ala Ala
188 -20                -15                -10
191 Ala Thr Ser Leu Ala Ser Pro Leu Pro Gln Gln Gln Arg Tyr Gly Lys
192 -5                -1 1                5                10
195 Arg Ala Thr Ser Asp Asp Trp Lys Ser Lys Ala Ile Tyr Gln Leu Leu
196                15                20                25

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199 Thr Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn
200      30      35      40
203 Leu Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu
204      45      50      55
207 Asp Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile
208 60      65      70      75
211 Pro Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe
212      80      85      90
215 Tyr Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala Leu
216      95      100      105
219 Ile Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val Val
220      110      115      120
223 Ala Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe
224      125      130      135
227 Gly Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asp
228 140      145      150      155
231 Gln Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile
232      160      165      170
235 Asp Thr Glu Asn Ser Asp Asn Val Ala Ile Leu Asn Asp Ile Val Ser
236      175      180      185
239 Gly Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val
240      190      195      200
243 Lys His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala Gly
244      205      210      215
247 Val Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly
248 220      225      230      235
251 Pro Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr Tyr
252      240      245      250
255 Ala Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile
256      255      260      265
259 Ser Glu Met Leu Gly Ser Asn Arg Asn Ala Phe Glu Asp Thr Ser Val
260      270      275      280
263 Leu Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser
264      285      290      295
267 Gln Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu
268 300      305      310      315
271 Gly Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser
272      320      325      330
275 Gly Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn Tyr
276      335      340      345
279 Asp Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val
280      350      355      360
283 Arg Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly Asp
284      365      370      375
287 Asn Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn
288 380      385      390      395
291 Tyr Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys
292      400      405      410
295 Phe Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr

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```

296          415          420          425
299 Thr Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly Leu
300          430          435          440
303 Pro Ala Ile Phe Thr Ser Ala
304          445          450
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 32
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Primer 168/R.p. amy3-forw
315 <400> SEQUENCE: 5
316 gaagatctac catgaaattc agcatctctc tc
319 <210> SEQ ID NO: 6
320 <211> LENGTH: 30
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Primer 169/R.p. amy4-rev
327 <400> SEQUENCE: 6
328 ccgctcgagt taagcagagg tgaagatagc

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,396

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Input Set : A:\PTO.AMC.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date